

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga
Guegler, Karl J.
Shah, Purvi
- (ii) TITLE OF THE INVENTION: HUMAN RETINOID BINDING PROTEIN
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0349 US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: SYNORAT01

(B) CLONE: 367304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Pro	Pro	Asn	Leu	Thr	Gly	Tyr	Tyr	Arg	Phe	Val	Ser	Gln	Lys	Asn
1			5					10					15		
Met	Glu	Asp	Tyr	Leu	Gln	Ala	Leu	Asn	Ile	Ser	Leu	Ala	Val	Arg	Lys
		20						25					30		
Thr	Ala	Leu	Leu	Lys	Pro	Asp	Lys	Glu	Ile	Glu	His	Gln	Gly	Asn	
		35					40				45				
His	Met	Thr	Val	Arg	Thr	Leu	Ser	Thr	Phe	Arg	Asn	Tyr	Thr	Val	Gln
	50					55				60					
Phe	Asp	Val	Gly	Val	Glu	Phe	Glu	Glu	Asp	Leu	Arg	Ser	Val	Asp	Gly
65				70					75					80	
Arg	Lys	Cys	Gln	Thr	Ile	Val	Thr	Trp	Glu	Glu	Glu	His	Leu	Val	Cys
			85					90					95		
Val	Gln	Lys	Gly	Glu	Val	Pro	Asn	Arg	Gly	Trp	Arg	His	Trp	Leu	Glu
		100					105					110			
Gly	Glu	Met	Leu	Tyr	Leu	Glu	Leu	Thr	Ala	Arg	Asp	Ala	Val	Cys	Glu
		115				120					125				
Gln	Val	Phe	Arg	Lys	Val	Arg									
	130					135									

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 957 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: SYNORAT01

(B) CLONE: 367304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGTGGAGCT	GGCTGGAATC	TCTCAGCCTC	ACCTGCCAGA	CAACACCCCC	TCCTTCCTCA	60
CCCTGTCTCC	TGCATTCTCC	TGAAACCTTC	ATCCACACAA	TGCCTCCCAA	CCTCACTGGC	120
TACTACCGCT	TTGTCTCGCA	GAAGACATG	GAGGACTACC	TGCAAGCCCT	AAACATCAGC	180
TTGGCTGTGC	GGAAGACCGC	GCTGCTGCTG	AAGCCGGACA	AGGAGATCGA	ACACCAGGGC	240
AACCACATGA	CGGTGAGGAC	GCTCAGCACC	TTCCGAAACT	ACACTGTGCA	GTTTGATGTG	300
GGAGTGGAGT	TTGAGGAGGA	CCTCAGGAGC	GTGGACGGAC	GAAAATGCCA	GACCATAGTA	360
ACCTGGGAGG	AGGAGCACCT	GGTGTGTGTG	CAGAAAGGGG	AGGTCCCCAA	CCGGGGCTGG	420
AGACACTGGC	TGGAGGGAGA	GATGCTGTAT	CTGGAAGTGA	CTGCAAGGGA	TGCAGTGTGC	480
GAGCAGGTCT	TCAGGAAGGT	CAGATAGCCG	GAGAGGAGCC	AAGATCCCTC	CAGACAGCAC	540
CAGCTCACAG	ACGCTCTTGT	TGTGCCCCCT	TCAAGCCCAG	ATTGTGCCAG	GTCAGCTGTC	600
CCTTCCTCTG	GCCACCTTTC	CTCCCTCTGG	GTCCCTCCTC	ACCCCTCCCC	GTGTTAATCT	660
GTAACCTGCA	GCCCCCAGGC	CAAAGTCCTT	TCTCACACTC	CACTGCCCAA	TAGTGACCTC	720
ACTTCCAGGT	CAAGGTCTGG	CGTCCCAAAT	GAAAGAAGCA	GGCAAAGGGA	AGGAGCCCCCT	780

GAGAACAACC AATCTCCGCT CTCTCCTGTC CATTGACCT CTTCTTTTCC TTCTAAGAAA	840
GAACTAAGCT TTGGGCATTT GGCGATTAGT GAAAATTCTA TCCTGATGGA CTTCTGGAAA	900
ACTGTGACTG GGGTTCAAGA GTTTAAACAG GGGCTACTGG CAGAGANAAA AAAAAAA	957

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 50548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Pro	Val	Asp	Phe	Asn	Gly	Tyr	Trp	Lys	Met	Leu	Ser	Asn	Glu	Asn
1				5					10					15	
Phe	Glu	Glu	Tyr	Leu	Arg	Ala	Leu	Asp	Val	Asn	Val	Ala	Leu	Arg	Lys
			20					25					30		
Ile	Ala	Asn	Leu	Leu	Lys	Pro	Asp	Lys	Glu	Ile	Val	Gln	Asp	Gly	Asp
			35					40					45		
His	Met	Ile	Ile	Arg	Thr	Leu	Ser	Thr	Phe	Arg	Asn	Tyr	Ile	Met	Asp
			50					55				60			
Phe	Gln	Val	Gly	Lys	Glu	Phe	Glu	Glu	Asp	Leu	Thr	Gly	Ile	Asp	Asp
65					70					75				80	
Arg	Lys	Cys	Met	Thr	Val	Ser	Trp	Asp	Gly	Asp	Lys	Leu	Gln	Cys	
				85					90				95		
Val	Gln	Lys	Gly	Glu	Lys	Glu	Gly	Arg	Gly	Trp	Thr	Gln	Trp	Ile	Glu
			100					105					110		
Gly	Asp	Glu	Leu	His	Leu	Glu	Met	Arg	Ala	Glu	Gly	Val	Ile	Cys	Lys
			115					120					125		
Gln	Val	Phe	Lys	Lys	Val	His									
			130					135							

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 190948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Pro	Val	Asp	Phe	Thr	Gly	Tyr	Trp	Lys	Met	Leu	Val	Asn	Glu	Asn
1				5					10					15	
Phe	Glu	Glu	Tyr	Leu	Arg	Ala	Leu	Asp	Val	Asn	Val	Ala	Leu	Arg	Lys

[illegible]

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